

AMENDMENTS TO THE CLAIMS

1. (Original) Factor RecA with an amino acid sequence that is at least identical to 96% of the amino acid sequence listed in SEQ ID NO. 2.
2. (Currently amended) ~~Factor~~ The factor according to claim 1 with an amino acid sequence that is ~~increasingly preferably identical to~~ at least 96.5%, ~~97%, 97.5%, 98%, 98.5%, 99%, 99.5% and quite particularly preferably 100%~~ identical to the amino acid sequence listed in SEQ ID No. 2.
3. (Original) Factor RecA, encoded from a nucleic acid, whose nucleotide sequence is at least 85% identical with the nucleotide sequence listed in SEQ ID NO. 1.
4. (Currently amended) The factor ~~Factor~~ according to claim 3, encoded from a nucleic acid, whose nucleotide sequence is ~~increasingly preferably identical to~~ at least 87.5%, ~~90%, 92.5%, 95%, 96%, 97%, 98%, 99% and quite particularly preferably 100%~~ identical of the nucleotide sequence listed in SEQ ID No. 1.
5. (Original) Nucleic acid encoding for a factor RecA, whose nucleotide sequence is at least 85% identical with the nucleotide sequence listed in SEQ ID NO. 1.
6. (Currently amended) The nucleic ~~Nucleic~~ acid according to claim 5, whose nucleotide sequence is ~~increasingly preferably identical to~~ at least 87.5%, ~~90%, 92.5%, 95%, 96%, 97%, 98%, 99% and quite particularly preferably 100%~~ identical of identical to the nucleotide sequence listed in SEQ ID NO. 1.
7. (Currently amended) The nucleic ~~Nucleic~~ acid according to claim 5 ~~or 6~~, encoding for a factor RecA, wherein the amino acid sequence is at least identical to 96% of the amino acid sequence listed in SEQ ID NO: 2 according to one of claims 1 to 4.
8. (Currently amended) A method of functionally inactivating ~~Use of nucleic acid that encodes for a factor RecA for the functional inactivation~~ of the gene *recA* in a gram-positive

bacterium that is not *Bacillus megaterium*, said method comprising the step of inactivating said *recA* gene with a nucleic acid sequence that encodes a factor RecA.

9. (Currently amended) The method of claim 8 ~~Use according to claim 8~~, wherein a nucleic acid that encodes for a non-active protein is introduced with a point mutation.

10. (Currently amended) The method of claim 8 ~~Use according to claim 8~~, wherein a nucleic acid with a deletion mutation or insertion mutation is employed, preferably comprising each of the boundary sequences that comprise at least 70 to 150 nucleic acid positions of the region encoding for the protein.

11. (Currently amended) The method of claim 8 ~~Use according to claim 8~~, wherein nucleic acids with a total of two nucleic acid segments are employed that each comprise at least 70 to 150 nucleic acid positions and thereby at least partially, preferably completely flank the region encoding for the protein.

12. (Canceled)

13. (Currently amended) The method of claim 8 ~~Use according to one of claims 8 to 12~~, wherein the gram-positive bacterium, ~~preferably one of the genera *Clostridium* or *Bacillus*~~, is naturally capable of sporulation and a gene from the phase IV of the sporulation is simultaneously functionally inactivated with *recA*.

14. (Currently amended) The method of claim 13 ~~Use according to claim 13~~, wherein the inactivated gene from the phase IV sporulation in the nomenclature of *B. subtilis* concerns one of the genes *spoIVA*, *spoIVB*, *spoIVCA*, *spoIVCB*, *spoIVFA*, *spoIVFB* or *yqfD* or homologue thereof ~~concerns a homologous gene to this, preferably in the case of *B. subtilis* the gene is *yqfD*, in the case of *Bacillus licheniformis* is the gene *spoIV* and in all other cases is a homologous gene to this.~~

15. (Currently amended) The method of claim 13 ~~Use according to claim 13 or 14~~, wherein exactly one gene from the phase IV of the sporulation is functionally inactivated.

16. (Currently amended) The method of claim 14 ~~Use according to claim 14 or 15~~, wherein the functional inactivation of the genes *spoIVA*, *spoIVB*, *spoIVCA*, *spoIVCB*, *spoIVFA*, *spoIVFB*, *yqfD* or *spoIV* or of each of their homologous genes occurs with the help of the sequences SEQ ID NO. 3, 5, 7, 9, 11, 13, 15 or 17 or parts thereof, ~~preferably with the help of parts that comprise at least 70 to 150 contiguous nucleic acid positions, particularly preferably with the help of two such parts that surround a part of the gene located between them.~~

17. (Currently amended) A gram-positive ~~Gram-positive~~ bacterium that is not *Bacillus megaterium* in which the gene *recA* is functionally inactivated.

18. (Currently amended) The gram-positive ~~Gram-positive~~ bacterium according to claim 17, wherein the functional inactivation is effected through point mutagenesis, partial deletion or insertion or total deletion of the encoding region for the complete protein.

19. (Currently amended) The gram-positive ~~Gram-positive~~ bacterium of claim 17 ~~according to claim 17 or 18~~, wherein the functional inactivation is effected through a nucleic acid which comprises a nucleotide sequence at least 85% identical to SEQ ID NO: 1. ~~according to one of claims 5 to 7 and/or a nucleic acid whose nucleotide sequence matches with the nucleotide sequence listed in SEQ ID NO. 31 in the positions 369 to 1415 to at least 1045, preferably at least 1046, quite particularly preferably 1047 of these 1047 positions, or is effected through the at least partially non-encoding flanking regions to these nucleic acids.~~

20. (Currently amended) The gram-positive ~~Gram-positive~~ bacterium of claim 17, wherein said bacterium ~~according to one of claims 17 to 19, preferably one of the genera *Clostridium* or *Bacillus*, which~~ is naturally capable of sporulation and by which a gene from the phase IV of the sporulation is simultaneously functionally inactivated with *recA*.

21. (Currently amended) The gram-positive ~~Gram-positive~~ bacterium according to claim 20, wherein the inactivated gene from the phase IV of the sporulation in the nomenclature of *B. subtilis* concerns one of the genes *spoIVA*, *spoIVB*, *spoIVCA*, *spoIVCB*, *spoIVFA*, *spoIVFB* or *yqfD* or homologue thereof ~~concerns a homologous gene to this, preferably in the case of *B.*~~

~~*subtilis* the gene is *yqfD*, in the case of *Bacillus licheniformis* is the gene *spoIV* and in all other cases is a homologous gene to this.~~

22. (Currently amended) The gram-positive ~~Gram-positive~~ bacterium of claim 20 ~~according to claim 20 or 21~~, wherein exactly one gene from the phase IV of the sporulation is functionally inactivated.

23. (Currently amended) The gram-positive ~~Gram-positive~~ bacterium of claim 21 ~~according to claim 21 or 22~~, wherein the functional inactivation of the genes *spoIVA*, *spoIVB*, *spoIVCA*, *spoIVCB*, *spoIVFA*, *spoIVFB*, *yqfD* or *spoIV* or of each of their homologous genes is effected with the help of the sequences SEQ ID NO. 3, 5, 7, 9, 11, 13, 15 or 17 or parts thereof; ~~preferably with the help of parts that comprise at least 70 to 150 contiguous nucleic acid positions, particularly preferably with the help of two such parts that surround a part of the gene located between them.~~

24. (Currently amended) The gram-positive ~~Gram-positive~~ bacterium of claim 17 ~~according to one of claims 17 to 23, wherein said bacterium is from~~ it concerns one of the genera *Clostridium* or *Bacillus*, ~~in particular one of the species *Bacillus subtilis*, *B. licheniformis*, *B. amyloliquefaciens*, *B. stearothermophilus*, *B. globigii*, *B. clausii* or *B. lentus*, and quite particularly a strain of *B. licheniformis*.~~

25. (Currently amended) A process ~~Process~~ for fermenting a gram-positive bacterium ~~according to one of claims 17 to 24 comprising the step of fermenting a gram-positive bacterium~~ of claim 17.

26. (Currently amended) The process ~~Process~~ according to claim 25 ~~for the manufacture of a product of value, in particular~~, wherein said gram-positive bacterium produces a low molecular weight compound or a protein.

27. (Currently amended) The process ~~Process~~ according to claim 26, wherein the low molecular weight compound ~~concerns~~ is a natural product, a nutritional supplement or a pharmaceutically relevant compound.

28. (Currently amended) The process ~~Process~~ according to claim 26, wherein the protein ~~concerns is~~ is an enzyme, ~~in particular an enzyme from the group of the α -amylases, proteases, cellulases, lipases, oxidoreductases, peroxidases, laccases, oxidases and hemicellulases.~~

29. (Currently amended) Use of the factor RecA of claim 1 ~~according to one of claims 1 to 4 and/or a RecA that matches with the amino acid sequence listed in SEQ ID NO. 32 in at least 347, preferably 348 of the 348 amino acid positions shown there,~~ in a molecular biological reaction approach.

30. (Currently amended) Use according to claim 29 for stabilizing single stranded DNA, ~~particularly in a DNA polymerization, in recombination processes *in vitro*, or for converting double stranded DNA into single stranded DNA or vice versa.~~

31. (Currently amended) A vector ~~Vector~~, comprising the ~~a~~ nucleic acid of claim 5 ~~according to one of claims 5 to 7.~~

32. (Currently amended) The vector ~~Vector~~ according to claim 31, wherein said vector is it ~~concerns an expression vector.~~

33. (Currently amended) A process ~~Process~~ for the manufacture of a factor RecA of claim 1 ~~according to one of claims 1 to 4.~~

34. (Currently amended) The process ~~Process~~ according to claim 33, under addition of a the nucleic acid of claim 1 to a host cell ~~according to one of claims 5 to 7, preferably an expression vector according to claim 32, further preferably by fermentation of a host comprising this nucleic acid or these expression vectors.~~

35. (Currently amended) Use of the nucleic acid encoding for a factor RecA of claim 1 ~~according to one of claims 1 to 4~~ for expressing this factor.

36. (Currently amended) Use according to claim 34 ~~claim 35~~ to manufacture this factor itself, ~~particularly in a process according to claim 34,~~ or to modulate molecular biological activities of the cells in ~~question, in particular in~~ recombination processes *in vivo*.

37. (Currently amended) Use of the nucleic acid encoding for a the factor RecA of claim 5 ~~according to one of claims 5 to 7 and/or a nucleic acid encoding for a factor RecA whose nucleotide sequence matches with the nucleotide sequence listed in SEQ ID NO. 31 in positions 369 to 1415 to at least 1045, preferably at least 1046, particularly preferably 1047 of these 1047 positions~~, for the inactivation of this factor of the gene *recA* in an *in vitro* approach, ~~in particular~~ through interaction with an associated nucleic acid.

38. (Canceled)

39. (Original) Use of at least one, preferably at least two nucleic acids orientated against one another according to SEQ ID NO. 25 to 30 for the amplification of an *in vivo* DNA region enclosed thereby.

40. (Original) Use according to claim 39 for the amplification of a *recA* gene.

41. (Currently amended) Use according to claim 39 ~~or 40~~ in the context of a process of claim 8 ~~according to one of claims 8 to 16~~.

42. (Currently amended) Use according to claim 39 ~~one of claims 39 to 41~~ for the production of a gram-positive bacterium of claim 17 ~~according to one of claims 17 to 24~~.

43. (Canceled)

44. (Canceled)

45. (Currently amended) Use according to claim 39 ~~claim 44~~ for the amplification of a *spoIV* gene.

46. (Currently amended) Use according to claim 45 ~~claim 44 or 45~~ in the context of a process according to claim 13 ~~one of claims 13 to 16~~.

47. (Currently amended) Use according to claim 45 ~~one of claims 44 to 46~~ for the production of a gram-positive bacterium according to claim 20 ~~one of claims 20 to 24~~.

48. (New) The method of claim 8, wherein said nucleic acid sequence comprises a nucleotide sequence at least 85% identical to SEQ ID NO: 1.